

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 11/658,344
Source: IFwp
Date Processed by STIC: 1/31/07

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IFWP

RAW SEQUENCE LISTING
PATENT APPLICATION: US/11/658,344

DATE: 01/31/2007
TIME: 08:34:24

Input Set : A:\SEQUENCE LISTING.txt
Output Set: N:\CRF4\01312007\K658344.raw

3 <110> APPLICANT: Novartis AG
 5 <120> TITLE OF INVENTION: Organic Compound
 7 <130> FILE REFERENCE: 4-33392P1
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/11/658,344
 C--> 9 <141> CURRENT FILING DATE: 2007-01-24
 9 <160> NUMBER OF SEQ ID NOS: 23
 11 <170> SOFTWARE: PatentIn version 3.2
 13 <210> SEQ ID NO: 1
 14 <211> LENGTH: 5
 15 <212> TYPE: PRT
 16 <213> ORGANISM: artificial
 18 <220> FEATURE:
 19 <223> OTHER INFORMATION: CDR1 region of AIN457
 22 <220> FEATURE:
 23 <221> NAME/KEY: DOMAIN
 24 <222> LOCATION: (1)..(5)
 25 <223> OTHER INFORMATION: CDR1 = hypervariable region 1 of heavy chain of AIN457
 27 <400> SEQUENCE: 1
 29 Asn Tyr Trp Met Asn
 30 1 5
 33 <210> SEQ ID NO: 2
 34 <211> LENGTH: 17
 35 <212> TYPE: PRT
 36 <213> ORGANISM: artificial
 38 <220> FEATURE:
 39 <223> OTHER INFORMATION: CDR2 of AIN457
 42 <220> FEATURE:
 43 <221> NAME/KEY: DOMAIN
 44 <222> LOCATION: (1)..(17)
 45 <223> OTHER INFORMATION: CDR2 = hypervariable region 2 of heavy chain of AIN457
 47 <400> SEQUENCE: 2
 49 Ala Ile Asn Gln Asp Gly Ser Glu Lys Tyr Tyr Val Gly Ser Val Lys
 50 1 5 10 15
 53 Gly
 57 <210> SEQ ID NO: 3
 58 <211> LENGTH: 18
 59 <212> TYPE: PRT
 60 <213> ORGANISM: artificial
 62 <220> FEATURE:
 63 <223> OTHER INFORMATION: CDR3 of AIN457
 66 <220> FEATURE:
 67 <221> NAME/KEY: DOMAIN
 68 <222> LOCATION: (1)..(18)

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69 <223> OTHER INFORMATION: CDR3 = hypervariable region 3 of heavy chain of AIN457
71 <400> SEQUENCE: 3
73 Asp Tyr Tyr Asp Ile Leu Thr Asp Tyr Tyr Ile His Tyr Trp Tyr Phe
74 1 5 10 15
77 Asp Leu
81 <210> SEQ ID NO: 4
82 <211> LENGTH: 12
83 <212> TYPE: PRT
84 <213> ORGANISM: artificial
86 <220> FEATURE:
87 <223> OTHER INFORMATION: CDR1' of AIN457
90 <220> FEATURE:
91 <221> NAME/KEY: DOMAIN
92 <222> LOCATION: (1)..(12)
93 <223> OTHER INFORMATION: CDR1' = hypervariable region 1 of light chain of AIN457
95 <400> SEQUENCE: 4
97 Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala
98 1 5 10
101 <210> SEQ ID NO: 5
102 <211> LENGTH: 7
103 <212> TYPE: PRT
104 <213> ORGANISM: artificial
106 <220> FEATURE:
107 <223> OTHER INFORMATION: CDR2' of AIN457
110 <220> FEATURE:
111 <221> NAME/KEY: DOMAIN
112 <222> LOCATION: (1)..(7)
113 <223> OTHER INFORMATION: CDR2' = hypervariable region 2 of light chain AIN457
115 <400> SEQUENCE: 5
117 Gly Ala Ser Ser Arg Ala Thr
118 1 5
121 <210> SEQ ID NO: 6
122 <211> LENGTH: 9
123 <212> TYPE: PRT
124 <213> ORGANISM: artificial
126 <220> FEATURE:
127 <223> OTHER INFORMATION: CDR3' of AIN457
130 <220> FEATURE:
131 <221> NAME/KEY: DOMAIN
132 <222> LOCATION: (1)..(9)
133 <223> OTHER INFORMATION: CDR3' = hypervariable region 3 of light chain AIN457
135 <400> SEQUENCE: 6
137 Gln Gln Tyr Gly Ser Ser Pro Cys Thr
138 1 5
141 <210> SEQ ID NO: 7
142 <211> LENGTH: 381
143 <212> TYPE: DNA
144 <213> ORGANISM: Homo sapiens
147 <220> FEATURE:

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148 <221> NAME/KEY: CDS
149 <222> LOCATION: (1)..(381)
150 <223> OTHER INFORMATION: DNA of heavy chain domain of AIN457
152 <400> SEQUENCE: 7
153 gag gtg cag ttg gtg gag tct ggg gga ggc ttg gtc cag cct ggg ggg 48
154 Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Gln Pro Gly Gly
155 1 5 10 15
157 tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt agt aac tat 96
158 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
159 20 25 30
161 tgg atg aac tgg gtc cgc cag gct cca ggg aaa ggg ctg gag tgg gtg 144
162 Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
163 35 40 45
165 gcc gcc ata aac caa gat gga agt gag aaa tac tat gtg ggc tct gtg 192
166 Ala Ala Ile Asn Gln Asp Gly Ser Glu Lys Tyr Tyr Val Gly Ser Val
167 50 55 60
169 aag ggc cga ttc acc atc tcc aga gac aac gcc aag aac tca ctg tat 240
170 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
171 65 70 75 80
173 ctg caa atg aac agc ctg aga gtc gag gac acg gct gtg tat tac tgt 288
174 Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Val Tyr Tyr Cys
175 85 90 95
177 gtg agg gac tat tac gat att ttg acc gat tat tac atc cac tat tgg 336
178 Val Arg Asp Tyr Tyr Asp Ile Leu Thr Asp Tyr Tyr Ile His Tyr Trp
179 100 105 110
181 tac ttc gat ctc tgg ggc cgt ggc acc ctg gtc act gtc tcc tca 381
182 Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser
183 115 120 125
186 <210> SEQ ID NO: 8
187 <211> LENGTH: 127
188 <212> TYPE: PRT
189 <213> ORGANISM: Homo sapiens
191 <400> SEQUENCE: 8
193 Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Gln Pro Gly Gly
194 1 5 10 15
197 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
198 20 25 30
201 Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
202 35 40 45
205 Ala Ala Ile Asn Gln Asp Gly Ser Glu Lys Tyr Tyr Val Gly Ser Val
206 50 55 60
209 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
210 65 70 75 80
213 Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Val Tyr Tyr Cys
214 85 90 95
217 Val Arg Asp Tyr Tyr Asp Ile Leu Thr Asp Tyr Tyr Ile His Tyr Trp
218 100 105 110
221 Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser
222 115 120 125

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Input Set : A:\SEQUENCE LISTING.txt
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225 <210> SEQ ID NO: 9
226 <211> LENGTH: 327
227 <212> TYPE: DNA
228 <213> ORGANISM: Homo sapiens
231 <220> FEATURE:
232 <221> NAME/KEY: CDS
233 <222> LOCATION: (1)..(327)
234 <223> OTHER INFORMATION: DNA of varibale part of light chain of AIN457
236 <400> SEQUENCE: 9
237 gaa att gtg ttg acg cag tct cca ggc acc ctg tct ttg tct cca qgg 48
238 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
239 1 5 10 15
241 gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt agc agc agc 96
242 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
243 20 25 30
245 tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctc ctc 144
246 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
247 35 40 45
249 atc tat ggt gca tcc agc agg gcc act ggc atc cca gac agg ttc agt 192
250 Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
251 50 55 60
253 ggc agt ggg tct ggg aca gac ttc act ctc acc atc agc aga ctg gag 240
254 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
255 65 70 75 80
257 cct gaa gat ttt gca gtg tat tac tgt cag cag tat ggt agc tca ccg 288
258 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
259 85 90 95
261 tgc acc ttc ggc caa ggg aca cga ctg gag att aaa cga 327
262 Cys Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
263 100 105
266 <210> SEQ ID NO: 10
267 <211> LENGTH: 109
268 <212> TYPE: PRT
269 <213> ORGANISM: Homo sapiens
271 <400> SEQUENCE: 10
273 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
274 1 5 10 15
277 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
278 20 25 30
281 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
282 35 40 45
285 Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
286 50 55 60
289 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
290 65 70 75 80
293 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
294 85 90 95
297 Cys Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
298 100 105

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Input Set : A:\SEQUENCE LISTING.txt

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301 <210> SEQ ID NO: 11
302 <211> LENGTH: 10
303 <212> TYPE: PRT
304 <213> ORGANISM: artificial
306 <220> FEATURE:
307 <223> OTHER INFORMATION: CDR1-x of AIN457
310 <220> FEATURE:
311 <221> NAME/KEY: DOMAIN
312 <222> LOCATION: (1)..(10)
313 <223> OTHER INFORMATION: CDR1-x = hypervariable domain x of heavy chain of AIN457
315 <400> SEQUENCE: 11
317 Gly Phe Thr Phe Ser Asn Tyr Trp Met Asn
318 1 5 10
321 <210> SEQ ID NO: 12
322 <211> LENGTH: 11
323 <212> TYPE: PRT
324 <213> ORGANISM: artificial
326 <220> FEATURE:
327 <223> OTHER INFORMATION: CDR2-x of AIN457
330 <220> FEATURE:
331 <221> NAME/KEY: domain
332 <222> LOCATION: (1)..(11)
333 <223> OTHER INFORMATION: CDR2-x = hypervariable domain of heavy chain x of AIN457
335 <400> SEQUENCE: 12
337 Ala Ile Asn Gln Asp Gly Ser Glu Lys Tyr Tyr
338 1 5 10
341 <210> SEQ ID NO: 13
342 <211> LENGTH: 23
343 <212> TYPE: PRT
344 <213> ORGANISM: artificial
346 <220> FEATURE:
347 <223> OTHER INFORMATION: CDR3-x of AIN457
350 <220> FEATURE:
351 <221> NAME/KEY: domain
352 <222> LOCATION: (1)..(23)
353 <223> OTHER INFORMATION: CDR3-x = hypervariable domain x of heavy chain AIN457
355 <400> SEQUENCE: 13
357 Cys Val Arg Asp Tyr Tyr Asp Ile Leu Thr Asp Tyr Tyr Ile His Tyr
358 1 5 10 15
361 Trp Tyr Phe Asp Leu Trp Gly
362 20
365 <210> SEQ ID NO: 14
366 <211> LENGTH: 20
367 <212> TYPE: DNA
368 <213> ORGANISM: artificial
370 <220> FEATURE:
371 <223> OTHER INFORMATION: Primer for cloning of heavy chain of AIN457
374 <220> FEATURE:
375 <221> NAME/KEY: primer_bind

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 01/31/2007
PATENT APPLICATION: US/11/658,344 TIME: 08:34:26

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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,5,6,11,12,13,14,15,16,17,18,19,20,21,22,23

VERIFICATION SUMMARY

PATENT APPLICATION: **US/11/658,344**

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Input Set : **A:\SEQUENCE LISTING.txt**

Output Set: **N:\CRF4\01312007\K658344.raw**

L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date